



<110> Brian Seed  
Tara Pouyan

<120> P-SELECTIN LIGANDS AND RELATED MOLECULES  
AND METHODS

<130> 00786/284002

<140> 08/756,018  
<141> 1996-11-25

<150> 60/000,213  
<151> 1995-06-14

<150> 08/661,960  
<151> 1996-06-12

<160> 17

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Val Thr

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<213> Homo sapiens

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Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp  
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Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro  
35 40

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Leu Pro Glu Thr  
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Leu Pro Glu Thr  
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Leu Pro Glu Ala  
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<210> 7  
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tcggtaagg tctcctgcaa ggcttctgaa ggcaccttca gcagctatgc tatcagctgg 180

gtgcgacagg cccctggaca agggctttag tggatggag ggatcatccc tatctttggt 240  
 acagcaaaact acgcacagaa gttccaggc agagtcacga ttaccgcgga cgaatccacg 300  
 agcacagcct acatggagct gagcagcctg agatctgagg acacggccgt gtattactgt 360  
 gcgagagata atggagcgta ttgttagtgg ggtagctgct actcgggctg gttcgacccc 420  
 tggggccagg gaaccctggt caccgtctct tcaggtgagt actgaattct agctttctgg 480  
 ggcaggccag gcctgacctt ggcttgggg cagggaggg gctaaggtaa ggcaggtggc 540  
 gccagcagg gcacacccaa tgcccatagag cccagacact ggacgctgaa cctcgccgac 600  
 agttaagaac ccagggccct ctgcgcctgg gcccagctct gtcccacacc ggggtcacat 660  
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 cgtccaccc catctttcc tcagcacctg aactcttggg gggaccgtca gtcttcctct 1560  
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 <211> 442  
 <212> PRT  
 <213> Homo sapiens

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 Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala  
 35 40 45  
 Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala  
 50 55 60  
 Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly  
 65 70 75 80  
 Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala  
 85 90 95  
 Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser  
 100 105 110  
 Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr

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Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
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Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val
145						150					155				160
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
					165					170				175	
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
				180						185				190	
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Asp	Lys
				195						200				205	
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
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Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
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Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
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Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
				260						265				270	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
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Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
		290				295						300			
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
305					310						315				320
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
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Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
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Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
				355						360				365	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
				370						375				380	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
385						390						395			400
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
					405						410			415	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
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Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
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<212> DNA
<213> Homo sapiens
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ggcaagttgt tttatatcgc atcggcctt cggaaacgagg agtacaataa gtcggttcag 180
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gggctgtctg tctatgtctg caagccagag acgaccaagg agcaactggg agagttctac 480
gaagctctcg actgcttgcg cattcccaag tcagatgtcg tgtacaccga ttggaaaaag 540
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gataagtgtg agccactgga gaagcagcac gagaaggaga ggaaacagga ggagggggaa 600  
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 cagccccagt ccagggcagc aaggcagcc ccgtctgcct cttcacccgg agcctctgcc 720  
 cggccccactc atgctcaggg agagggtctt ctggctttt cccaggctct gggcaggcac 780  
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 ctccctgtct ccgggtaaat gagtgcacg gccc 1894

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 <213> Homo sapiens

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 Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe Tyr Ile Ala Ser  
 35 40 45  
 Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln Glu Ile Gln Ala  
 50 55 60  
 Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu  
 65 70 75 80  
 Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr  
 85 90 95  
 Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly  
 100 105 110  
 Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr  
 115 120 125  
 Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val  
 130 135 140  
 Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr  
 145 150 155 160  
 Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp Val Val Tyr Thr  
 165 170 175  
 Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys Gln His Glu Lys  
 180 185 190  
 Glu Arg Lys Gln Glu Glu Gly Glu Ser Asp Pro Glu Gly Glu Pro Lys  
 195 200 205  
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
 210 215 220

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 225 230 235 240  
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 245 250 255  
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 260 265 270  
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser  
 275 280 285  
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 290 295 300  
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
 305 310 315 320  
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 325 330 335  
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln  
 340 345 350  
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 355 360 365  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 370 375 380  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 385 390 395 400  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
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 Leu Ser Pro Gly Lys  
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<210> 12  
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 <212> PRT  
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 Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala  
 35 40 45  
 Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala  
 50 55 60  
 Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly  
 65 70 75 80  
 Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala  
 85 90 95  
 Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser  
 100 105 110  
 Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr  
 115 120 125  
 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
 130 135 140  
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
 145 150 155 160  
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
 165 170 175

*(Handwritten marks: a large 'X' is on the left margin, and a small 'X' is below it, and a small 'U' is to the right of the 'X').*

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
180 185 190  
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys  
195 200 205  
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
210 215 220  
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
225 230 235 240  
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
245 250 255  
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Asn Phe Ser Trp  
260 265 270  
Tyr Val Asp Gly Val Glu Val His Asn Asn Lys Thr Lys Pro Arg Glu  
275 280 285  
Glu Asn Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
290 295 300  
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Asn Val Ser Asn  
305 310 315 320  
Lys Ala Leu Pro Ala Pro Ile Glu Lys Asn Ile Ser Lys Ala Lys Gly  
325 330 335  
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
340 345 350  
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
355 360 365  
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
370 375 380  
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
385 390 395 400  
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
405 410 415  
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
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<212> PRT  
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